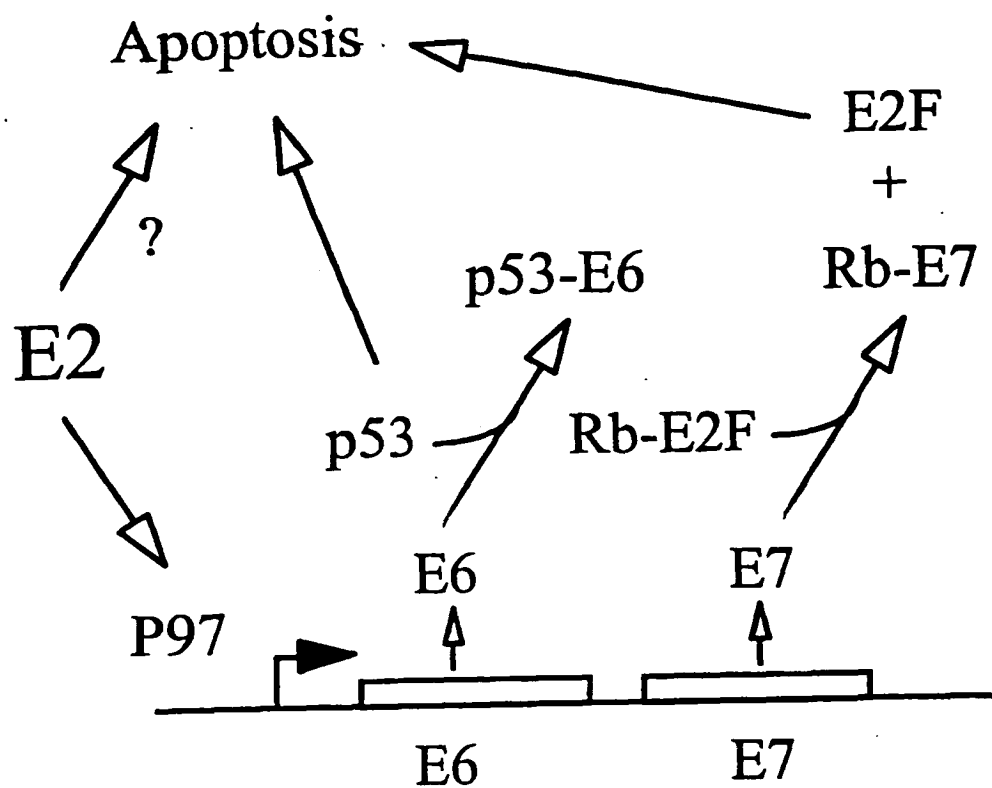


Fig. 1

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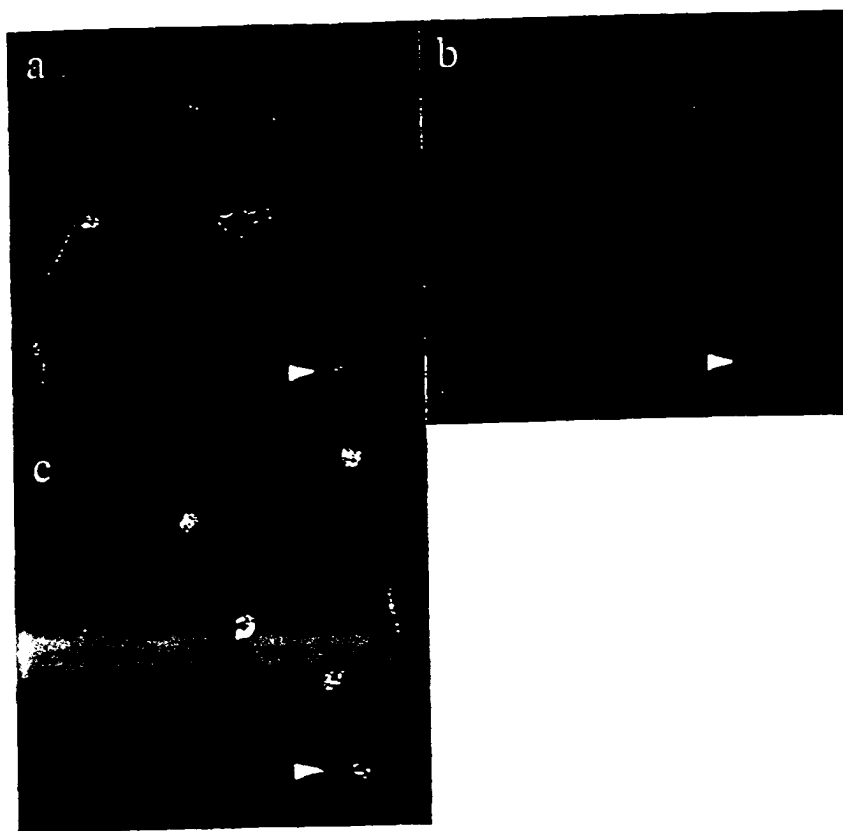
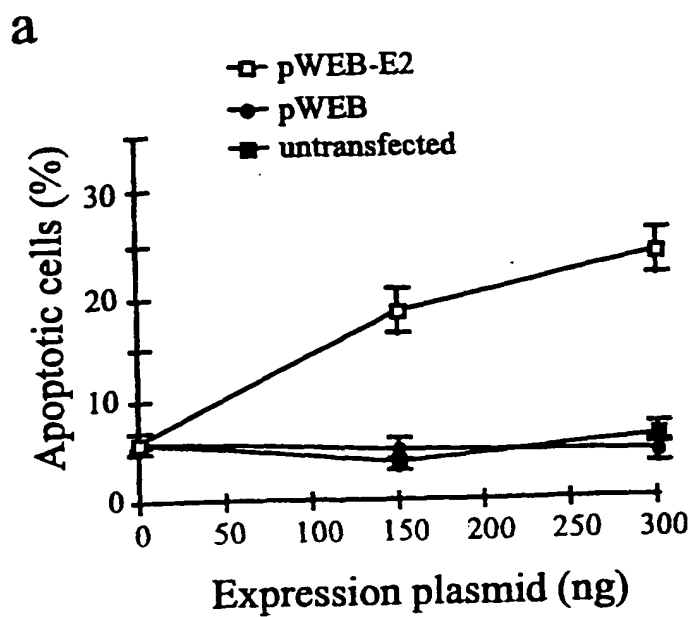


Fig. 2

204770-0662400T

Fig. 3A



204TFO-0654400T

b

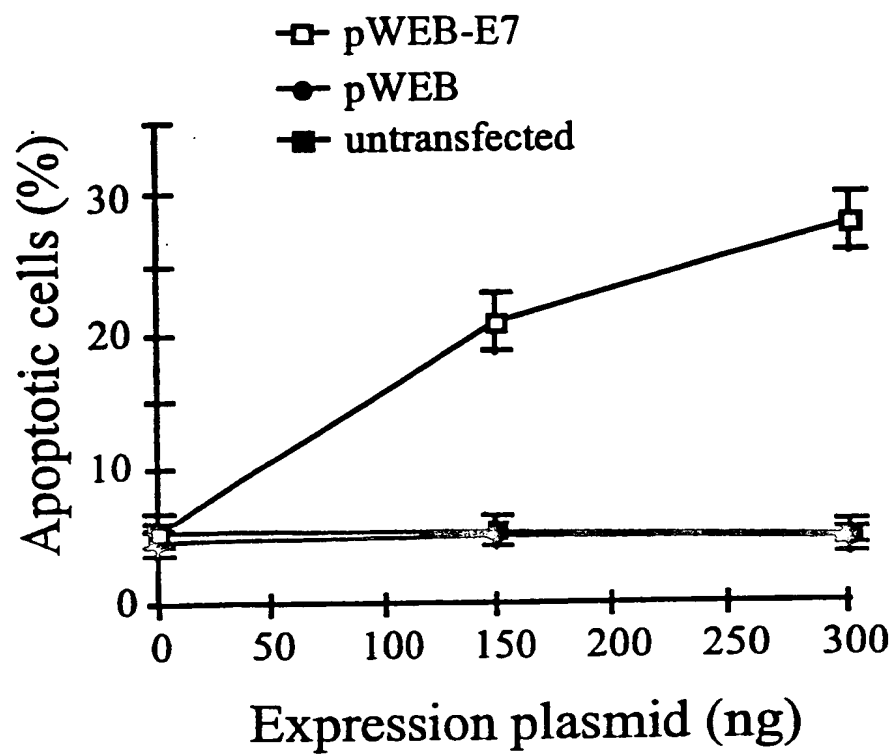


Fig. 3B

Fig. 4

a

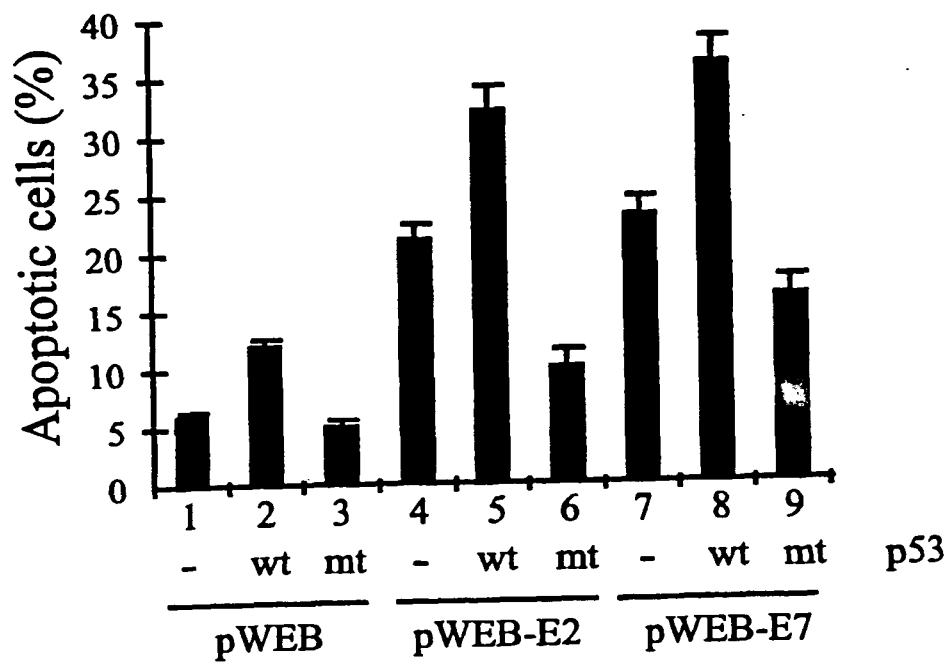
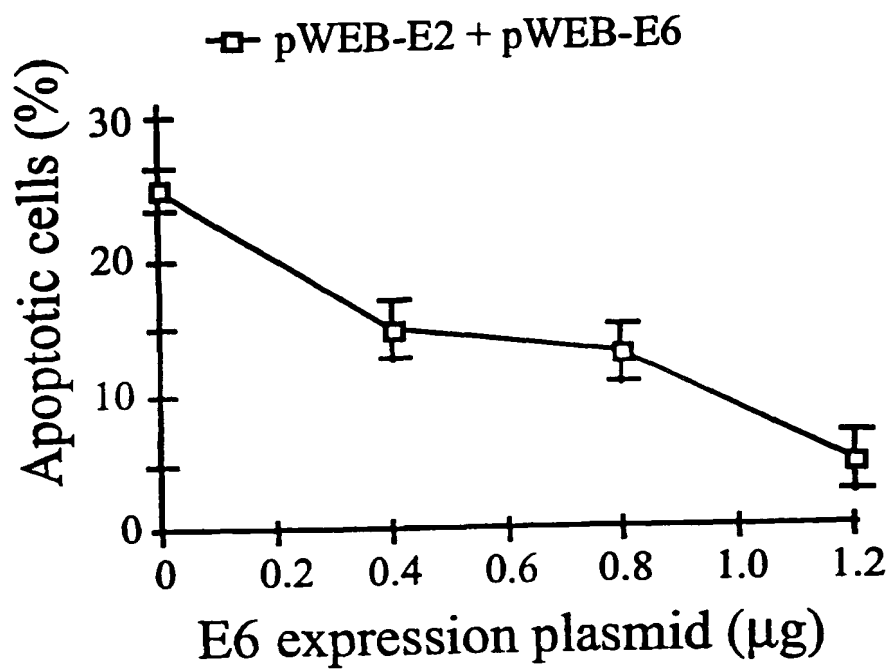


Fig. 4B

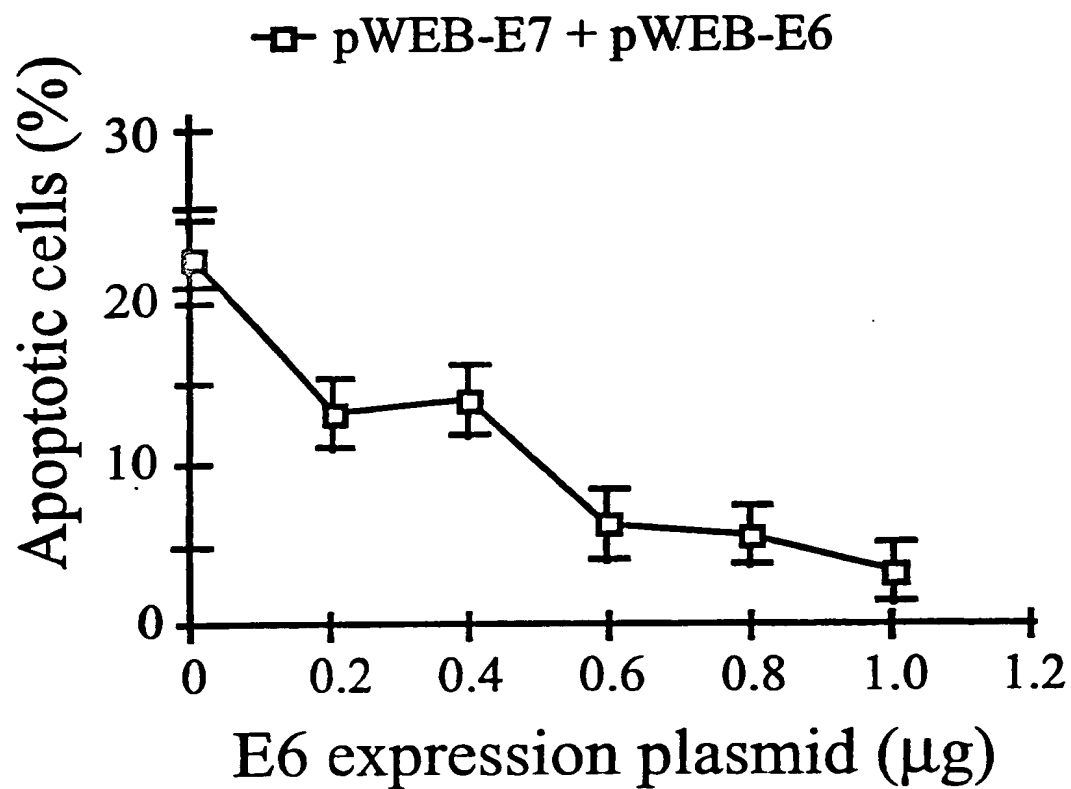
b



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Fig 4C

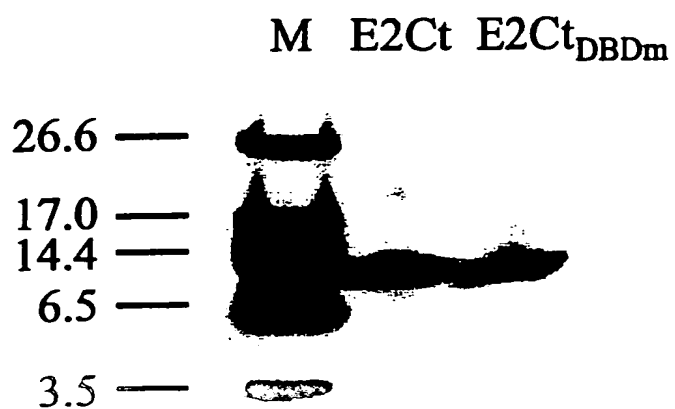
C



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Fig 5A

a



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Fig 5B

b

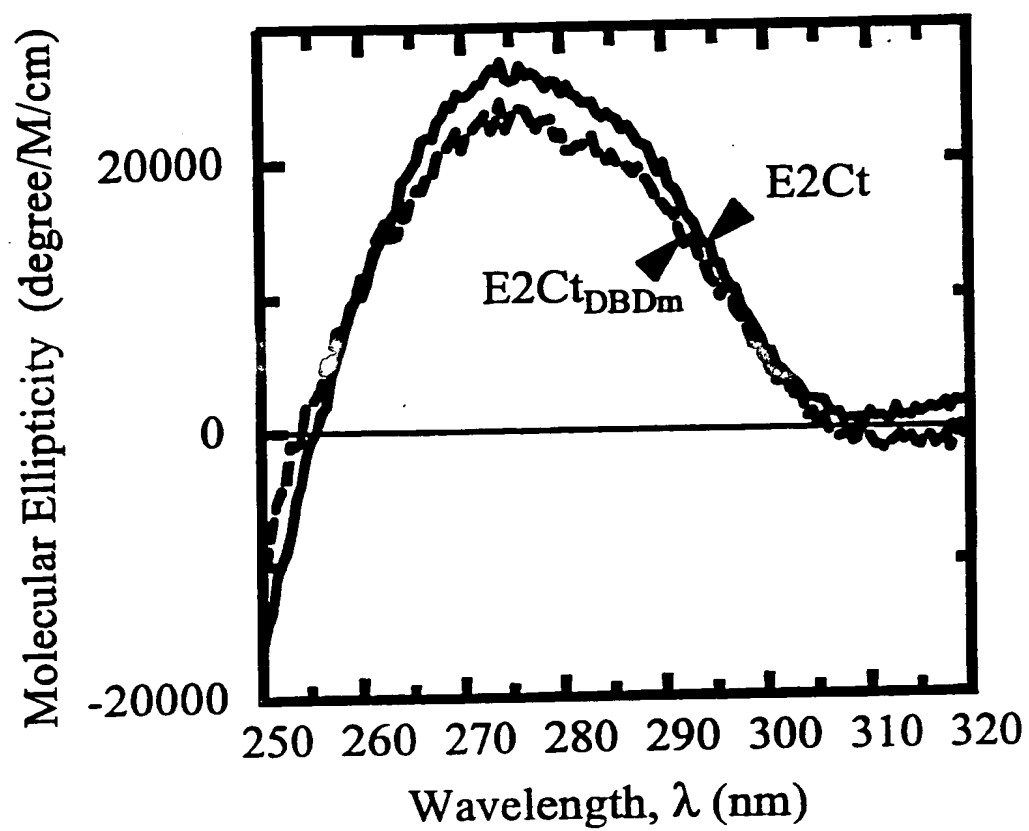


Fig 5C

C

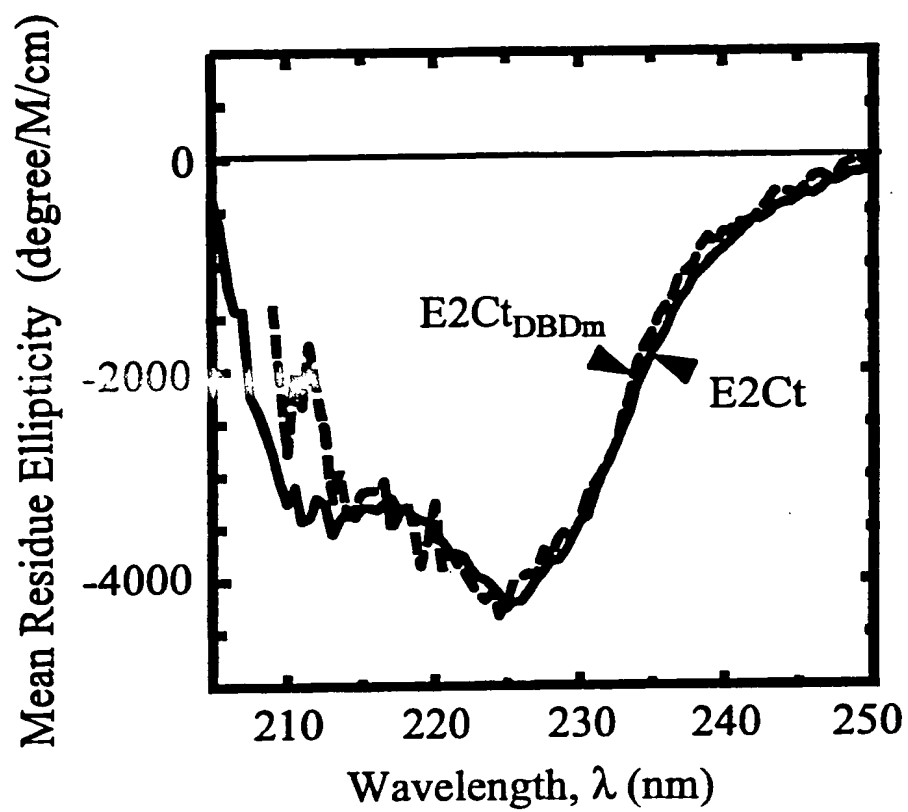
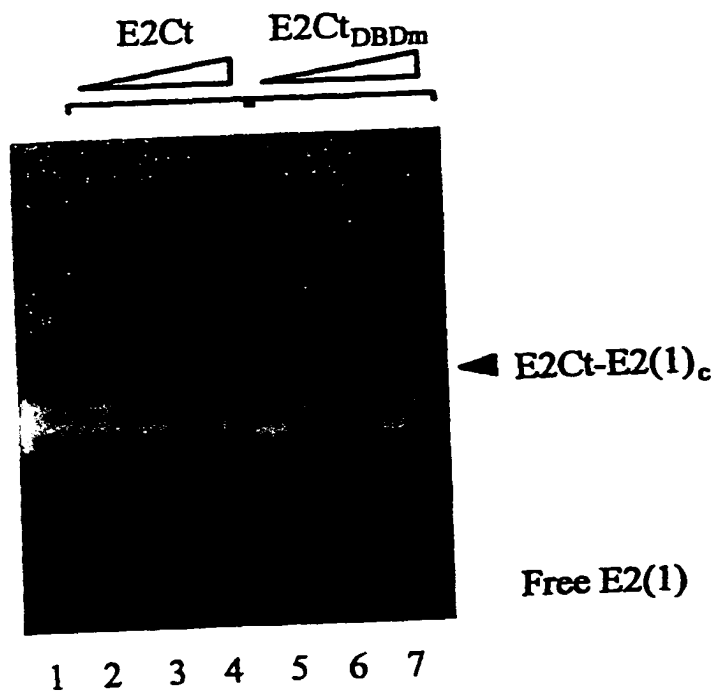


Fig 5D

d



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Fig. 6

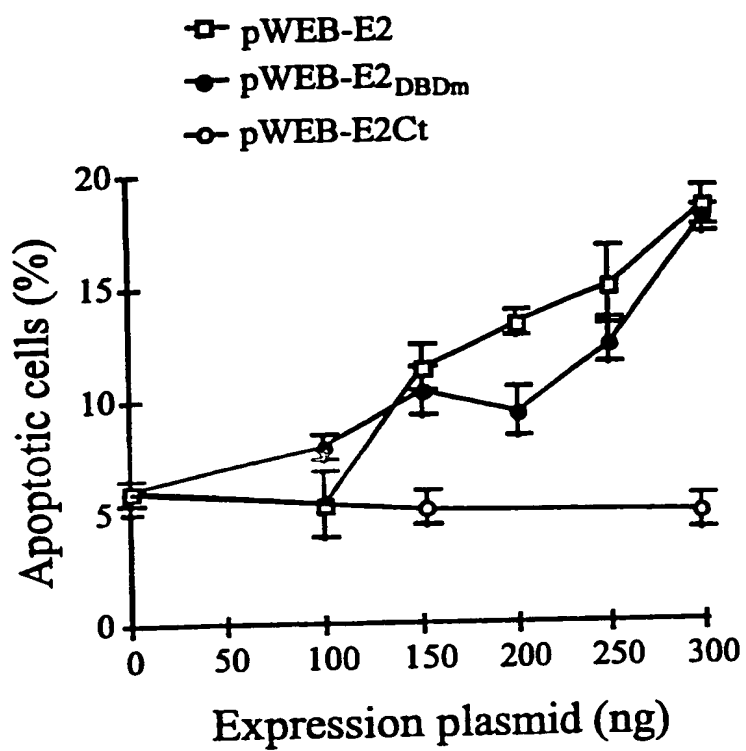
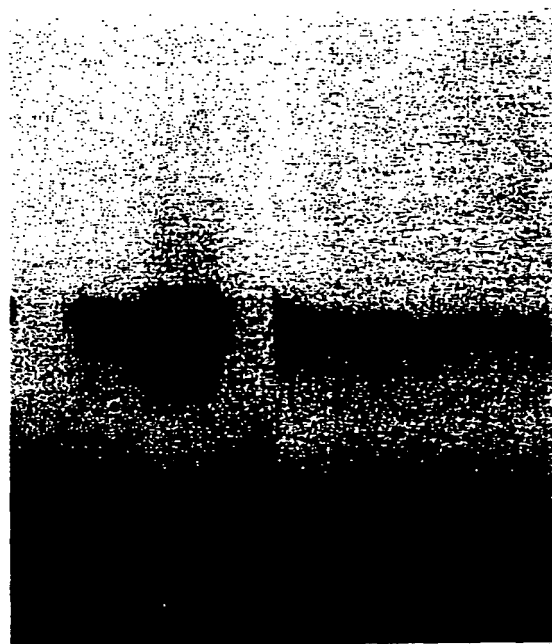


Fig. 7A

a

-	50	150	-	50	50	50	50	E2Ct (nM)
-	-	-	150	-	50	100	150	E2Ct _{DBDm} (nM)

◀ E2Ct-E2(1)_c

Free E2(1)

1 2 3 4 5 6 7 8

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Fig. 7B

b

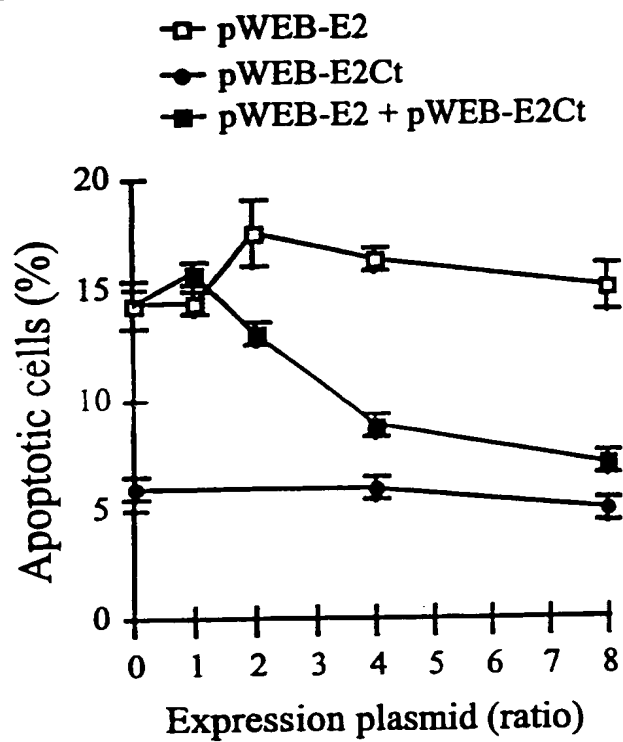


Fig. 8

The E2 proteins used in this work

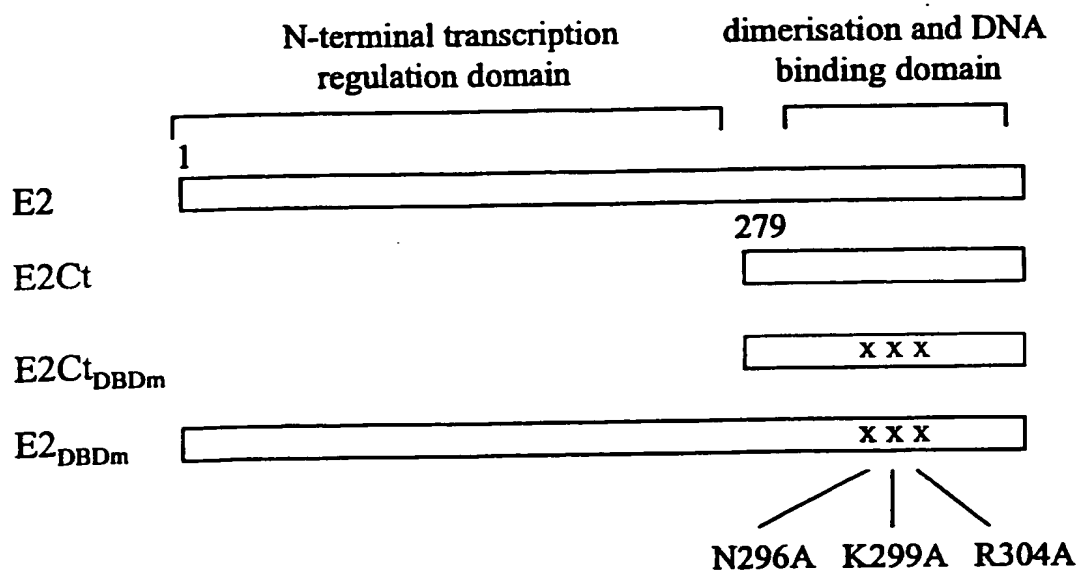


Fig. 9

HPV 16 E2

2755 ATGGAGACTCTTTGCCAACGTTTAAATGTGTGTCAGGACAAAATACTAACACATTATGAA
-----+-----+-----+-----+-----+-----+-----+-----
M E T L C Q R L N V C Q D K I L T H Y E

2815 AATGATAGTACAGACCTACGTGACCATATAGACTATTGGAAACACATGCGCCTAGAATGT
-----+-----+-----+-----+-----+-----+-----+-----
N D S T D L R D H I D Y W K H M R L E C

GCTATTTATTACAAGGCCAGAGAAATGGGATTTAAACATATTAACCACCAAGTGGTGCCA

2875 -----+-----+-----+-----+-----+-----+-----+-----
A I Y Y K A R E M G F K H I N H Q V V P

2935 ACACTGGCTGTATCAAAGAATAAAGCATTACAAGCAATTGAACTGCAACTAACGTTAGAA
-----+-----+-----+-----+-----+-----+-----+-----
T L A V S K N K A L Q A I E L Q L T L E

2995 ACAATATATAACTCACAATATAGTAATGAAAAGTGGACATTACAAGACGTTAGCCTTGAA
-----+-----+-----+-----+-----+-----+-----+-----
T I Y N S Q Y S N E K W T L Q D V S L E

3055 GTGTATTTAACTGCACCAACAGGATGTATAAAAAACATGGATATACAGTGAAGTGCAG
-----+-----+-----+-----+-----+-----+-----+-----
V Y L T A P T G C I K K H G Y T V E V Q

3115 TTTGATGGAGACATATGCAATACAATGCATTATACAACTGGACACATATATATATTTGT
-----+-----+-----+-----+-----+-----+-----+-----
F D G D I C N T M H Y T N W T H I Y I C

3175 GAAGAAGCATCAGTAACTGTGGTAGAGGGTCAAGTTGACTATTATGGTTTATATTATGTT
-----+-----+-----+-----+-----+-----+-----+-----
E E A S V T V V E G Q V D Y Y G L Y Y V

3235 CATGAAGGAATACGAACATATTTTGTGCAGTTTAAAGATGATGCAGAAAAATATAGTAA
-----+-----+-----+-----+-----+-----+-----+-----
H E G I R T Y F V Q F K D D A E K Y S K

3295 AATAAAGTATGGGAAGTTCATGCGGGTGGTCAGGTAATATTATGTCCTACATCTGTGTTT
-----+-----+-----+-----+-----+-----+-----+-----
N K V W E V H A G G Q V I L C P T S V F

3355 AGCAGCAACGAAGTATCCTCTCCTGAAATTATTAGGCAGCACTTGGCCAACCACCCCGCC
-----+-----+-----+-----+-----+-----+-----+-----
S S N E V S S P E I I R Q H L A N H P A

3415 GCGACCCATACCAAAGCCGTGCGCTTGGGCACCGAAGAAACACAGACGACTATCCAGCGA
-----+-----+-----+-----+-----+-----+-----+-----

10047990-011402

A T H T K A V A L G T E E T Q T T I Q R

3475 CCAAGATCAGAGCCAGACACCGGAAACCCCTGCCACACCACTAAGTTGTTGCACAGAGAC
-----+-----+-----+-----+-----+-----+-----
P R S E P D T G N P C H T T K L L H R D

3535 TCAGTGGACAGTGCTCCAATCCTCACTGCATTTAACAGCTCACACAAAGGACGGATTAAC
-----+-----+-----+-----+-----+-----+-----
S V D S A P I L T A F N S S H K G R I N

3595 TGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTAATACTTTAAAATGT
-----+-----+-----+-----+-----+-----+-----
C N S N T T P I V H L K G D A N T L K C

3655 TTAAGATATAGATTTAAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----
L R Y R F K K H C T L Y T A V S S T W H

3715 TGGACAGGACATAATGTAAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

3775 TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAACCTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

3835 GGATTTATGTCTATATGA 3852
-----+-----+-----
G F M S I * -

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Fig 10

HPV 16 E2DBDm

ATGGAGACTCTTTGCCAACGTTTAAATGTGTGTCAGGACAAAATACTAACACATTATGAA
2755 -----+-----+-----+-----+-----+-----+-----
M E T L C Q R L N V C Q D K I L T H Y E

AATGATAGTACAGACCTACGTGACCATATAGACTATTGGAAACACATGCGCCTAGAATGT
2815 -----+-----+-----+-----+-----+-----+-----
N D S T D L R D H I D Y W K H M R L E C

GCTATTTATTACAAGGCCAGAGAAATGGGATTTAAACATATTAACCACCAAGTGGTGCCA

2875 -----+-----+-----+-----+-----+-----+-----
A I Y Y K A R E M G F K H I N H Q V V P

ACACTGGCTGTATCAAAGAATAAAGCATTACAAGCAATTGAACTGCAACTAACGTTAGAA
2935 -----+-----+-----+-----+-----+-----+-----
T L A V S K N K A L Q A I E L Q L T L E

ACAATATATAACTCACAATATAGTAATGAAAAGTGGACATTACAAGACGTTAGCCTTGAA
2995 -----+-----+-----+-----+-----+-----+-----
T I Y N S Q Y S N E K W T L Q D V S L E

GTGTATTTAACTGCACCAACAGGATGTATAAAAAACATGGATATACAGTGAAGTGCAG
3055 -----+-----+-----+-----+-----+-----+-----
V Y L T A P T G C I K K H G Y T V E V Q

TTTGATGGAGACATATGCAATACAATGCATTATACAAACTGGACACATATATATTTGT
3115 -----+-----+-----+-----+-----+-----+-----
F D G D I C N T M H Y T N W T H I Y I C

GAAGAAGCATCAGTAACTGTGGTAGAGGGTCAAGTTGACTATTATGGTTTATATTATGTT
3175 -----+-----+-----+-----+-----+-----+-----
E E A S V T V V E G Q V D Y Y G L Y Y V

CATGAAGGAATACGAACATATTTTGTGCAGTTTAAAGATGATGCAGAAAAATATAGTAAA
3235 -----+-----+-----+-----+-----+-----+-----
H E G I R T Y F V Q F K D D A E K Y S K

AATAAGTATGGGAAGTTCATGCGGGTGGTCAGGTAATATTATGTCCTACATCTGTGTTT
3295 -----+-----+-----+-----+-----+-----+-----
N K V W E V H A G G Q V I L C P T S V F

AGCAGCAACGAAGTATCCTCTCCTGAAATTATTAGGCAGCACTTGGCCAACCACCCCGCC
3355 -----+-----+-----+-----+-----+-----+-----
S S N E V S S P E I I R Q H L A N H P A

GCGACCCATACCAAAGCCGTCGCCTTGGGCACCGAAGAAACACAGACGACTATCCAGCGA
3415 -----+-----+-----+-----+-----+-----+-----
A T H T K A V A L G T E E T Q T T I Q R

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CCAAGATCAGAGTCCAGACACCGGAAACCCCTGCCACACCCTAAGTTGTTGCACAGAGAC
 3475 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----
 P R S E P D T G N P C H T T K L L H R D

TCAGTGGACAGTGCTCCAATCCTCACTGCATTTAACAGCTCACACAAAGGACGGATTAAC
 3535 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----
 S V D S A P I L T A F N S S H K G R I N

TGTAATAGTAACACTACCCCATAGTACATTTAAAAGGTGATGCTgctACTTTAgcaTGT
 3595 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----
 C N S N T T P I V H L K G D A A T L A C

TTAAGATATgcaTTTAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTACATGGCAT
 3655 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----
 L R Y A F K K H C T L Y T A V S S T W H

TGGACAGGACATAATGTAAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
 3715 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----
 W T G H N V K H K S A I V T L T Y D S E

TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAACTATTACAGTGTCTACT
 3775 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----
 W Q R D Q F L S Q V K I P K T I T V S T

GGATTTATGTCTATATGA
 3835 -----+-----+----- 3852
 G F M S I * -

Fig 11

E2Ct

ATGAACTGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTAATACTTTAAATGT
-----+-----+-----+-----+-----+-----+-----+-----
M N C N S N T T P I V H L K G D A N T L K C

TTAAGATATAGATTTAAAAAGCATTGTACATTGTATACTGCAGTGTCTCGTCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----+-----
L R Y R F K K H C T L Y T A V S S T W H

TGGACAGGACATAATGTAAACATAAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAACTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

GGATTTATGTCTATATGA
-----+-----+-----+-----+-----+-----+-----+----- 3852
G F M S I * -

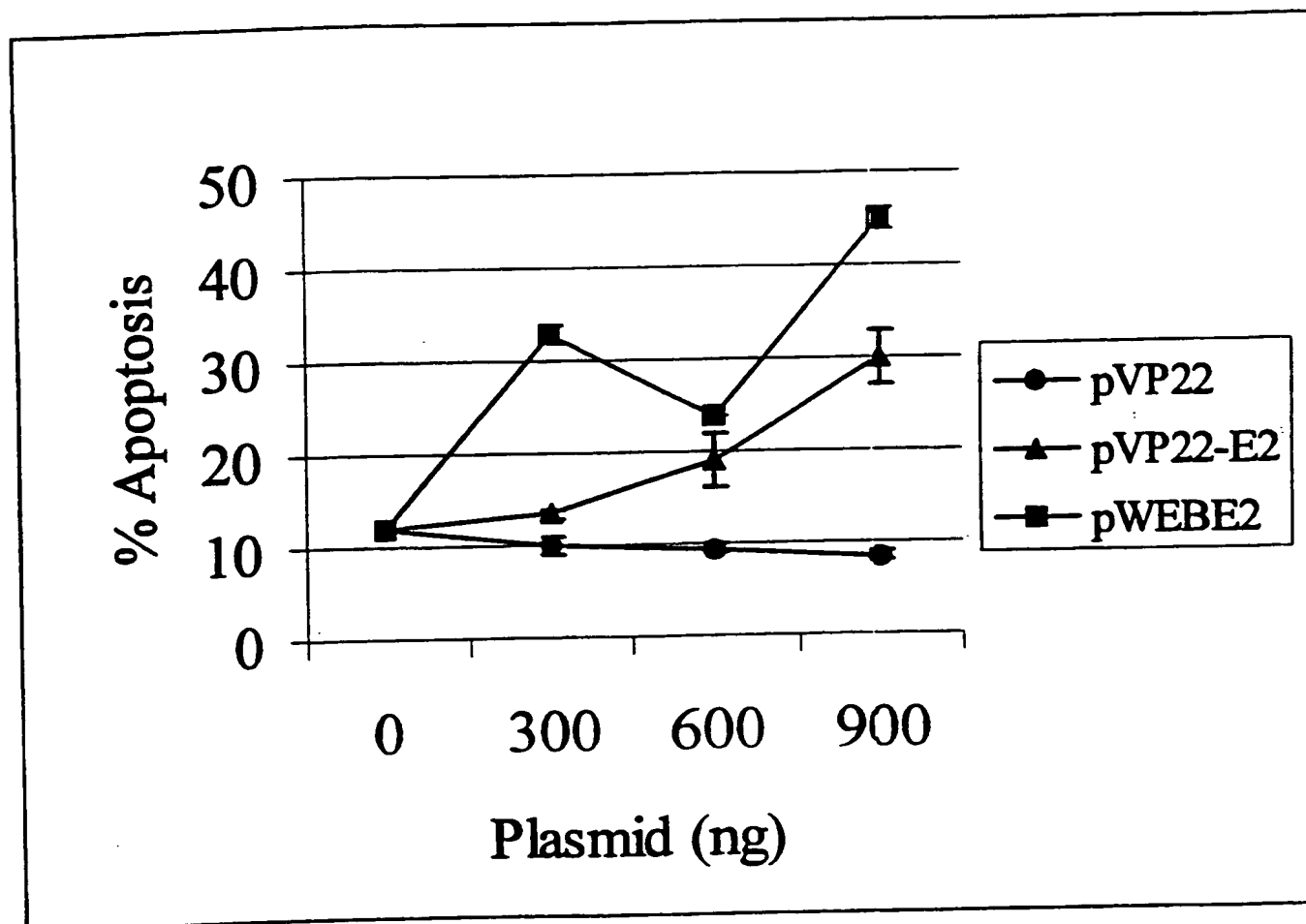
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E2CtD8Dm

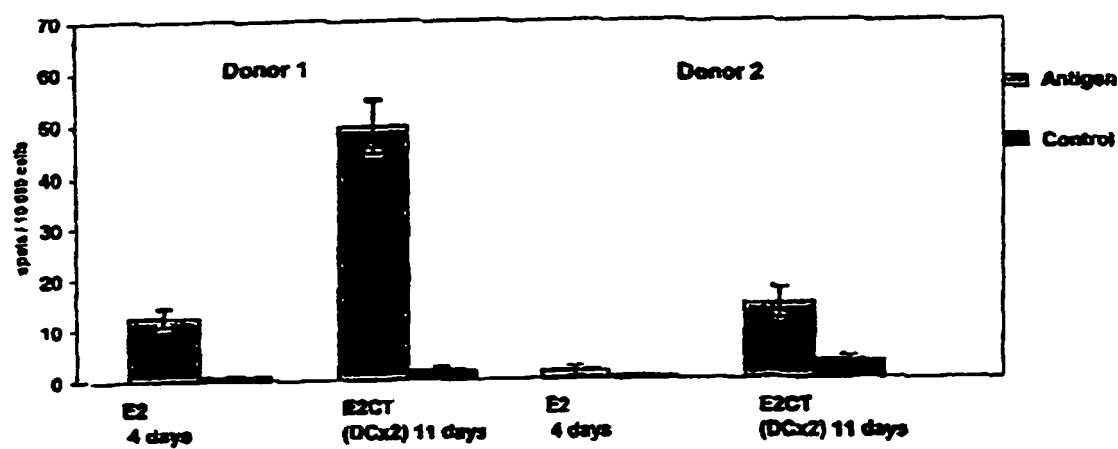
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Fig 13



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